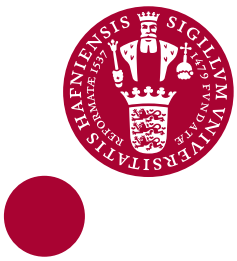

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Draft Genome Sequence of *Bacillus* sp. Strain K2I17, Isolated from the Rhizosphere of *Deschampsia antarctica* Desv.

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ABSTRACT We present here the draft genome sequence of *Bacillus* sp. strain K2I17, which was isolated from the rhizosphere of *Deschampsia antarctica* Desv. The genomic sequence contained 6,113,341 bp. This genome provides insights into the possible new biomedical and biotechnical applications of this specific Antarctic bacterium.

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The genus *Bacillus* is a phenotypically large, diverse collection of Gram-positive, endospore-forming, aerobic or facultatively anaerobic bacteria that have undergone considerable reclassification due to high phylogenetic heterogeneity (1). In addition, this genus is distributed widely in extreme environments and includes psychrophilic, thermophilic, acidophilic, alkalophilic, and halophilic bacteria that utilize a wide range of carbon sources for growth (2, 3).

Bacillus spp. comprise one of the most interesting groups of bacteria in biotechnology due to their resistance to pH and temperature changes, which are important parameters in industrial processes (4). To date, the presence of *Bacillus* spp. has been demonstrated in different environments, including the rhizosphere, the layer of soil influenced by plant-root metabolism. In comparison to root-free soil or bulk soil, the rhizosphere displays higher contents of nutrients, which could explain the activity of *Bacillus* spp. in these dynamic environments (5), and thus new approaches have begun to utilize the biotechnological applications of *Bacillus* and related species for agricultural and pharmaceutical products (6). Here, we announce the draft genome sequence of *Bacillus* sp. strain K2I17, which was isolated from the rhizosphere of *Deschampsia antarctica* Desv., at the Collins Glacier, Fildes Peninsula, King George Island, Antarctica (62°10′S, 58°55′W).

Bacillus sp. strain K2I17 was grown at 18°C in LB broth (catalog no. 12106-05; Mo Bio, Inc.). Genomic DNA was extracted using the Power Biofilm DNA isolation kit (catalog no. 24000-50; Mo Bio, Inc.) according to the manufacturer's protocol. A sequencing library was prepared using the Illumina HiSeq 2500 platform (Macrogene, Republic of Korea) with paired-end read sizes of 100 bp. A total of 15,092,729 paired-end reads were used for the *de novo* assembly in Geneious version 9.1.6 (7). Short and low-coverage contigs were filtered out, resulting in a set of 146 with an average coverage of 89× (N_{50}, 142,492 bp). Annotation was performed with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (8). Additionally, the genomes were analyzed on the Rapid Annotation using Subsystems Technology (RAST) server (9). Acquired antibiotic resistance genes were identified using ResFinder version 2.1 (10), virulence factors using virulencefinder version 1.2 (11), and prophage-related sequences using PHASTER (12).

The final assembly for *Bacillus* sp. strain K2I17 had a total length of 6,113,341 bp and a G+C content of 34.9%. Genome annotation resulted in 6,125 coding sequences (CDSs), 22 tRNAs, 326 pseudogenes, and 7 rRNAs; 59% of the CDSs were classified as hypothetical proteins. Five prophage-like elements between 19 and 36 kb were detected. Interestingly, one of them encodes a putative cell-adhesion protein. Genes resistant to the antibiotics tetracycline [*tet*(M) and *tet*(O)], penicillin (*bl*, *bla*, *ampS*, *pse2*, and *ybxI*), vancomycin (*vanA and vanH*), fosfomycin (*fosA*, *fosB*, and *fosX*), and fluoroquinolones (*parC* and *parE*) were detected. Also, secondary metabolism genes that encode thiazole/oxazole-modified microcin synthesis, auxin biosynthesis, pyridoxine (vitamin B_6) biosynthesis, and lanthionine biosynthesis were identified. In addition, 27 membrane-bound and secreted *Listeria* internalin-like proteins (LPXTG and GW motifs) were identified. Thus, this genome sequence can facilitate the understanding of the genetic diversity within the *Bacillus* genus, which could be useful for the development of new biotechnological applications.

Accession number(s). The draft genome sequence of *Bacillus* sp. strain K2I17 has been deposited in GenBank under the accession no. NJGF00000000. The version described in this paper is the first version, NJGF01000000.

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